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DOI: <https://doi.org/10.1038/nplants.2017.19>

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ZORA URL: <https://doi.org/10.5167/uzh-144175>

Journal Article

Accepted Version

Originally published at:

Krattinger, Simon G; Keller, Beat (2017). Resistance: Double gain with one gene. Nature Plants, 3:17019.

DOI: <https://doi.org/10.1038/nplants.2017.19>

RESISTANCE

Two in one sweep – a single rice gene improves multiple agronomic traits

The rice gene *Xa4* encodes a wall-associated kinase and controls disease resistance as well as mechanical strength possibly through a common mechanism.

Simon G. Krattinger and Beat Keller

Crop plants experience a wide range of stresses that negatively affect their performance. Rice, one of the most important global crops, is the main calorie source for more than half of the global population. Two of the major constraints in rice cultivation are bacterial diseases and lodging (Fig. 1). On page XXXX of this issue, Hu and colleagues unravel the identity and molecular function of the *Xa4* gene¹. This important disease resistance gene codes for a wall-associated kinase (WAK). The presence of *Xa4* confers resistance to bacterial blight and was found to strengthen the cell wall, which is a primary entry point for pathogens. Interestingly, the cell wall reinforcement also led to reduced height of *Xa4* expressing plants, thereby increasing lodging resistance. Hence, this gene has a beneficial effect on multiple agronomic traits, which can explain its importance and widespread use in rice breeding.

One of the 21st century's biggest challenges is to produce enough food for a growing world population. To ensure food security, breeding needs to focus on making crop plants more resilient to diseases, drought, flooding and other biotic and abiotic stresses. Bacterial blight is among the most damaging diseases of rice and the most sustainable strategy to protect rice from this villain is by exploring naturally occurring genetic resistance. Dozens of resistances against bacterial blight were described in different rice cultivars and landraces. However, the identity of the underlying genes, so called *Xa* genes, and their molecular function is only known for few of them. *Xa4* was introduced into commercial rice cultivars in the 1970s by the International Rice Research Institute and *Xa4* rice is nowadays cultivated in many countries where the gene continues to confer durable resistance against different strains of the bacterial blight pathogen. With the help of genetics, *Xa4* was previously delimited to a small region within the rice genome that contained several genes². Hu and colleagues now identified a WAK gene from the respective interval as *Xa4*. WAKs are cell surface-localized receptor kinases. Some of them form part of a sophisticated surveillance system that monitors the cell's surrounding for the presence of pathogen derived molecules. Transformation of the *Xa4* gene into a susceptible rice line reduced growth of bacterial blight, whereas RNAi-based silencing of *Xa4* increased susceptibility.

WAKs are composed of an extracellular ligand-binding domain, a membrane-spanning helix and a cytoplasmic kinase domain. In contrast to other receptor kinase families, WAKs have the ability to directly associate with the cell wall as it was demonstrated for *Xa4*. Interestingly, the presence of *Xa4* not only resulted in increased resistance against bacterial blight, but also in a reduction of plant height and increased strength of the cell wall. This cell wall reinforcement was caused by increased amounts of the major cell wall component cellulose and by reduced flexibility of the

cell wall. In order to elongate, plant cells rely on a flexible cell wall and cell wall strengthening can therefore explain the reduced height of *Xa4* expressing plants. Very importantly, the short plant stature and strong cell wall increased lodging resistance, without any detectable yield reduction. The reduction of plant height was a hallmark of the 'Green Revolution' and resulted in the replacement of tall low-yielding landraces with semi-dwarf cultivars. The reduced height of *Xa4* expressing plants was independent of pathogen infection, indicating that the gene has a constitutive activity. Inoculation with bacterial blight however induced *Xa4* expression more than 30 fold, which may lead to a further reinforcement of the cell wall after infection. The stronger cell wall might directly limit pathogen spreading because it is known that thickening of secondary cell walls in xylem parenchyma cells is an important component of bacterial blight resistance³. The bacterial blight pathogen mainly proliferates in the vascular tissue and eventually clogs it. Hence, the cell wall modification conferred by *Xa4* can explain both increased pathogen and lodging resistance. On the other hand, *Xa4* was also associated with increased levels of the defense hormone jasmonic acid-isoleucine and increased production of defense compounds. Whether the *Xa4*-mediated disease resistance is solely due to cell wall reinforcement, increased production of defense compounds or both needs to be determined.

It is interesting that the importance of WAKs for disease resistance was only recognized very recently by several independent studies⁴⁻⁸. Among them is the *Htn1* gene from maize that confers partial and broad-spectrum resistance against the fungal disease northern corn leaf blight⁴. Another example is the *Stb6* gene that confers race-specific resistance against the fungus *Zymoseptoria tritici* in wheat. The recent insight into WAK-based disease resistance offers the possibility to specifically explore this gene family for disease resistance breeding, for example through allele mining. Cereal genomes encode for over hundred WAKs and it is reasonable to assume that many more play a role in disease resistance. Whether WAK-based disease resistance is generally more durable or of broader-specificity than resistance conferred by other surface-localized receptor kinase families or intracellular immune receptors is an intriguing question that needs to be addressed in the future. The race-specific reactions of *Stb6* and *Xa4* indicate that certain pathogen strains are able to evade recognition by these WAKs, suggesting a similar gene-for-gene interaction as it was described for intracellular NLR immune proteins. The study of Hu and colleagues further highlights the importance of WAKs in pathogen defense. An important question that remains to be solved concerns the ligand that is perceived by *Xa4*. The reduced height, which develops independent of pathogen infection, might indicate that the *Xa4* ligand is a plant-derived molecule. Alternatively, this phenotype might be the result of 'leaky' signaling activity that occurs even in the absence of a ligand. In this case, the presence of a pathogen-derived ligand could further activate *Xa4* signaling. Classically, WAKs are associated with the perception of oligosaccharide ligands, for example cell wall components⁹. Interestingly, a recent study showed that WAKs can also perceive pathogen-derived peptides⁶. The example of *Xa4* is of particular interest because it provides an example where a single WAK affects both, pathogen defense and developmental processes probably through the same molecular mechanism. This offers the possibility to simultaneously improve resistances to multiple stresses in breeding through the introduction of a single gene.

1. Hu, K. *et al. Nature Plants* (2017).
2. Sun, X., Yang, Z., Wang, S. & Zhang, Q. *Theor Appl Genet* **106**, 683-687 (2003).
3. Nino-Liu, D.O., Ronald, P.C., Bogdanove A.J. *Mol Plant Pathol* **7**, 303-324 (2006).

4. Hurni, S. *et al. Proc Natl Acad Sci USA* **112**, 8780-8785 (2015).
5. Zuo, W. *et al. Nat Genet* **47**, 151-157 (2015).
6. Shi, G. *et al. Science Adv* **2**, e1600822 (2016).
7. Delteil, A. *et al. BMC Plant Biol* **16**, 17 (2016).
8. Saintenac *et al.* submitted
9. Kohorn, B.D. & Kohorn, S.L. *Front Plant Sci* **3**, 88 (2012).

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Figure 1. Lodging in a rice field (Picture was kindly provided by Suchit Prasad Shrestha, IRRI)